CHI GENOMICS UNIT CAPABILITIES

Assaying single cells for studying their transcriptome (scRNA-seq), cell surface proteome (CITE-seq), immune repertoire (BCR-/TCR-seq, Ag-specific B cell capture), as well as chromatin accessibility (scATAC-seq).

Thousands of cells are partitioned into nanoliter-scale Gel Beads-in-emulsion (GEMs), where all cDNA generated within a single droplet share a common 10x Barcode.

Libraries are generated and sequenced from the cDNA and the 10x Barcodes are used to associate each read back to its individual partition.

SINGLE-CELL RNA SEQUENCING (scRNA-SEQ)

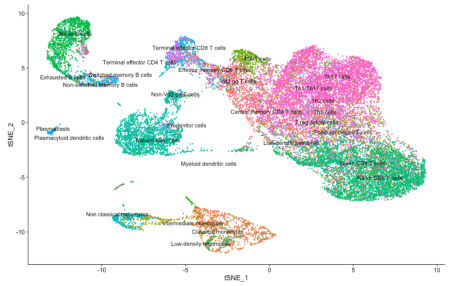
scRNA-seq enables studying the transcriptome at a single cell level to capture cellular heterogeneity in a sample. Here, Poly(dT) primer enables the production of barcoded, full-length cDNA from poly-adenylated mRNA that can be used for library generation and sequencing to obtain gene expression profile at a single cell level.

CELLULAR INDEXING OF TRANSCRIPTOMES AND EPITOPES BY SEQUENCING (CITE-SEQ)

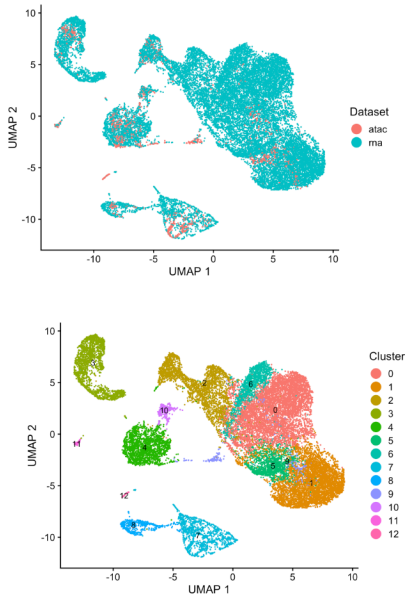
CITE-seq combines single-cell RNA sequencing (scRNA-seq) with detection of cell surface proteins, using oligo-labeled antibodies to enable more robust cell type discrimination. Here, along with the Poly(dT) primer that capture full-length cDNA from poly-adenylated mRNA, additional capture (primer) sequences are used for priming of Feature Barcodes (ADT-Antibody derived tags or Hashtags). Hashtags can be used to stain individual samples which can then be pooled and processed together to minimize batching effects.

IMMUNE PROFILING

BCR-/TCR-seq can be combined with scRNA-seq or CITE-seq to simultaneously investigate B- and T-cell repertoire and antigen specificity along with gene expression, and/or cell surface protein expression at a single cell level. Here, full-length (5' UTR to constant region), paired T-cell receptor (TCR) and/or B-cell receptor (BCR) transcripts derived from poly-adenylated mRNA are sequenced to obtain complete V(D)J sequences. Ag-specific B-cells can be selected and then used for BCR-seq.



Enabling robust cell type discrimination with CITE-seq



Data integration with scATAC-seq

ASSAY FOR TRANSPOSASE -ACCESSIBLE CHROMATIN USING SEQUENCING IN SINGLE CELLS (scATAC-SEQ)

scATAC-seq is used to obtain a genome-wide snapshot of chromatin accessibility. Here, a transposase is used to preferentially tag accessible DNA regions with sequencing adaptors. This enables assessment of chromatin changes associated with transcription at a single cell level.

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